



SUBSTITUTE SEQUENCE LISTING

<110> Falco, Saverio Carl
Famodu, Layo
Rafalski, Jan A.
Ramaker, Michael
Tarczynski, Mitchell C.
Thorpe, Catherine

<120> PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE
METHIONINE CONTENT OF THE SEEDS OF PLANTS

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Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Ser Ser Tyr
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Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Glu
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Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly Leu Ser Thr Tyr Phe Ser
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Lys Ala Leu Gly Ile Asp Thr Val Pro Val Leu Val Gly Pro Val Ser
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Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
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Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Leu Asp Glu Pro
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Tyr	Gly	Ala	Gly	Ile	Gly	Pro	Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Arg	690	695	700	
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Val	Leu	Glu	Lys	Asn	Ile	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	725	730	735	
Thr	Arg	Lys	Tyr	Thr	Glu	Val	Lys	Pro	Pro	Ser	Gln	Asn	Met	Val	Ala	740	745	750	
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<211> 2296

<212> DNA

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Asp Leu Lys Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
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Arg Tyr Asn Trp Ala Gly Gly Glu Ile Ala Phe Asp Thr Tyr Phe Ser
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Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
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Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asp Glu Tyr Lys Glu Ala
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Lys Gly Leu Gly Val Asp Thr Val Pro Val Leu Ile Gly Pro Val Ser
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Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Pro
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Leu Leu Ser Leu Leu Asp Lys Val Leu Pro Ile Tyr Lys Glu Val Ile
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Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
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Thr Leu Val Leu Asp Leu Gln Ala His Gln Leu Glu Ala Phe Thr Lys
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Glu	Thr	Tyr	Phe	Ala	Asp	Val	Pro	Ala	Glu	Ala	Phe	Lys	Thr	Leu	Thr	245	250	255	
Ala	Leu	Lys	Gly	Val	Thr	Ala	Phe	Gly	Phe	Asp	Leu	Val	Arg	Gly	Ala	260	265	270	
Gln	Thr	Leu	Asp	Leu	Ile	Lys	Gly	Gly	Phe	Pro	Ser	Gly	Lys	Tyr	Leu	275	280	285	
Phe	Ala	Gly	Val	Val	Asp	Gly	Arg	Asn	Ile	Trp	Ala	Asn	Asp	Leu	Ala	290	295	300	
Ala	Ser	Leu	Asn	Leu	Leu	Gln	Ser	Leu	Glu	Gly	Ile	Val	Gly	Lys	Asp	305	310	315	320
Lys	Leu	Val	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Thr	Ala	Val	Asp	325	330	335	
Leu	Val	Asn	Glu	Thr	Lys	Leu	Asp	Asp	Glu	Ile	Lys	Ser	Trp	Leu	Ala	340	345	350	
Phe	Ala	Ala	Gln	Lys	Val	Val	Glu	Val	Asn	Ala	Leu	Ala	Lys	Ala	Leu	355	360	365	
Ala	Gly	His	Lys	Asp	Glu	Ala	Phe	Phe	Ser	Ala	Asn	Ala	Thr	Ala	Gln	370	375	380	
Ala	Ser	Arg	Lys	Ser	Ser	Pro	Arg	Val	Thr	Asn	Glu	Ala	Val	Gln	Lys	385	390	395	400
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Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Val	Glu	Leu	Arg	Arg	435	440	445	
Val	Arg	Arg	Glu	Tyr	Lys	Ala	Lys	Lys	Ile	Ser	Glu	Glu	Glu	Tyr	Val	450	455	460	
Lys	Ala	Ile	Lys	Ala	Glu	Ile	Lys	Lys	Val	Val	Asp	Leu	Gln	Glu	Glu	465	470	475	480
Leu	Asp	Ile	Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	485	490	495	
Val	Glu	Tyr	Phe	Gly	Glu	Gln	Leu	Ser	Gly	Phe	Ala	Phe	Thr	Ala	Asn	500	505	510	
Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Lys	Pro	Pro	Ile	Ile	515	520	525	
Tyr	Gly	Asp	Val	Ser	Arg	Pro	Asn	Pro	Met	Thr	Val	Phe	Trp	Ser	Lys	530	535	540	

Thr	Ala	Gln	Ser	Met	Thr	Lys	Arg	Pro	Met	Lys	Gly	Met	Leu	Thr	Gly	545	550	555	560
Pro	Val	Thr	Ile	Leu	Asn	Trp	Ser	Phe	Val	Arg	Asn	Asp	Gln	Pro	Arg	565	570	575	
Phe	Glu	Thr	Cys	Tyr	Gln	Ile	Ala	Leu	Ala	Ile	Lys	Asp	Glu	Val	Glu	580	585	590	
Asp	Leu	Glu	Lys	Ala	Gly	Ile	Thr	Val	Ile	Gln	Ile	Asp	Glu	Ala	Ala	595	600	605	
Leu	Arg	Glu	Gly	Leu	Pro	Leu	Arg	Lys	Ala	Glu	His	Ala	Phe	Tyr	Leu	610	615	620	
Asn	Trp	Ala	Val	His	Ser	Phe	Arg	Ile	Thr	Asn	Val	Gly	Ile	Gln	Asp	625	630	635	640
Thr	Thr	Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Asn	Phe	Asn	Asp	Ile	645	650	655	
Ile	His	Ser	Ile	Ile	Asp	Met	Asp	Ala	Asp	Val	Ile	Thr	Ile	Glu	Asn	660	665	670	
Ser	Arg	Ser	Asp	Glu	Lys	Leu	Leu	Ser	Val	Phe	Arg	Glu	Gly	Val	Lys	675	680	685	
Tyr	Gly	Ala	Gly	Ile	Gly	Pro	Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Arg	690	695	700	
Ile	Pro	Ser	Thr	Glu	Glu	Ile	Ala	Asp	Arg	Val	Asn	Lys	Met	Leu	Ala	705	710	715	720
Val	Leu	Asp	Thr	Asn	Ile	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	725	730	735	
Thr	Arg	Lys	Tyr	Ala	Glu	Val	Lys	Pro	Ala	Leu	Glu	Asn	Met	Val	Ser	740	745	750	
Ala	Ala	Lys	Ala	Ile	Arg	Thr	Gln	Leu	Ala	Ser	Ser	Lys				755	760	765	

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 35 40 45
 Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
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 Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Asp
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Met	Xaa	Lys	Gly	Asn	Ala	Thr	Val	Pro	Ala	Met	Glu	Met	Thr	Lys	Trp
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35 40 45
Ile Gly Ser Phe Pro Gln Thr Met Asp Leu Arg Arg Val Arg Arg Glu
50 55 60

Tyr Lys Ala Lys Glu Asp Leu Xaa Xaa Gly Val Cys Gln Cys Tyr Gln
 65 70 75 80
 Gly Arg Asn Xaa Gln Arg Leu Ser Arg Phe Lys Glu Glu Leu Asp Ile
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 35 40 45
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 50 55 60
 Tyr Asp Gln Val Leu Asp Thr Ala Thr Met Leu Gly Ala Val Pro Pro
 65 70 75 80
 Arg Tyr Asn Phe Ala Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
 85 90 95
 Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
 100 105 110
 Phe Asp Thr Asn Tyr His Tyr Ile Val Pro Glu Leu Gly Pro Glu Val
 115 120 125
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 130 135 140
 Lys Glu Leu Gly Val Asp Thr Val Pro Val Leu Val Gly Pro Val Thr
 145 150 155 160
 Phe Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Thr Phe Pro
 165 170 175
 Leu Leu Ser Leu Leu Asp Lys Ile Leu Pro Val Tyr Lys Glu Val Ile
 180 185 190
 Gly Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
 195 200 205
 Thr Leu Val Leu Asp Leu Glu Ser His Gln Leu Glu Ala Phe Thr Lys
 210 215 220

Ala	Tyr	Ser	Glu	Leu	Glu	Ser	Thr	Leu	Ser	Gly	Leu	Asn	Val	Ile	Val	225	230	235	240
Glu	Thr	Tyr	Phe	Ala	Asp	Ile	Pro	Ala	Glu	Thr	Tyr	Lys	Ile	Leu	Thr		245	250	255
Ala	Leu	Lys	Gly	Val	Thr	Gly	Phe	Gly	Phe	Asp	Leu	Val	Arg	Gly	Ala		260	265	270
Lys	Thr	Leu	Asp	Leu	Ile	Lys	Gly	Gly	Phe	Pro	Ser	Gly	Lys	Tyr	Leu		275	280	285
Phe	Ala	Gly	Val	Val	Asp	Gly	Arg	Asn	Ile	Trp	Ala	Asn	Asp	Leu	Ala		290	295	300
Ala	Ser	Leu	Ser	Thr	Leu	Gln	Ser	Leu	Glu	Gly	Ile	Val	Gly	Lys	Asp		305	310	315
Lys	Leu	Val	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Thr	Ala	Val	Asp		325	330	335
Leu	Val	Asn	Glu	Pro	Lys	Leu	Asp	Lys	Glu	Ile	Lys	Ser	Trp	Leu	Ala		340	345	350
Phe	Ala	Ala	Gln	Lys	Val	Val	Glu	Val	Asn	Ala	Leu	Ala	Lys	Ala	Leu		355	360	365
Ala	Gly	Glu	Lys	Asp	Glu	Ala	Phe	Phe	Ser	Glu	Asn	Ala	Ala	Ala	Gln		370	375	380
Ala	Ser	Arg	Lys	Ser	Ser	Pro	Arg	Val	Thr	Asn	Gln	Ala	Val	Gln	Lys		385	390	395
Ala	Ala	Ala	Ala	Leu	Arg	Gly	Ser	Asp	His	Arg	Arg	Ala	Thr	Thr	Val		405	410	415
Ser	Ala	Arg	Leu	Asp	Ala	Gln	Gln	Lys	Lys	Leu	Asn	Leu	Pro	Val	Leu		420	425	430
Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Leu	Glu	Leu	Arg	Arg		435	440	445
Val	Arg	Arg	Glu	Tyr	Lys	Ala	Lys	Lys	Ile	Ser	Glu	Asp	Asp	Tyr	Val		450	455	460
Lys	Ala	Ile	Lys	Glu	Glu	Ile	Ser	Lys	Val	Val	Lys	Leu	Gln	Glu	Glu		465	470	475
Leu	Asp	Ile	Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met		485	490	495
Val	Glu	Tyr	Phe	Gly	Glu	Gln	Leu	Ser	Gly	Phe	Ala	Phe	Thr	Ala	Asn		500	505	510
Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Lys	Pro	Pro	Ile	Ile		515	520	525
Tyr	Gly	Asp	Val	Ser	Arg	Pro	Asn	Pro	Met	Thr	Val	Phe	Trp	Ser	Gln		530	535	540

Thr	Ala	Gln	Ser	Met	Thr	Lys	Arg	Pro	Met	Lys	Gly	Met	Leu	Thr	Gly	545	550	555	560
Pro	Val	Thr	Ile	Leu	Asn	Trp	Ser	Phe	Val	Arg	Asn	Asp	Gln	Pro	Arg	565	570	575	
Phe	Glu	Thr	Cys	Tyr	Gln	Ile	Ala	Leu	Ala	Ile	Lys	Asp	Glu	Val	Glu	580	585	590	
Asp	Leu	Glu	Lys	Ala	Gly	Ile	Asn	Val	Ile	Gln	Ile	Asp	Glu	Ala	Ala	595	600	605	
Leu	Arg	Glu	Gly	Leu	Pro	Leu	Arg	Lys	Ala	Glu	His	Ala	Phe	Tyr	Leu	610	615	620	
Asp	Trp	Ala	Val	His	Ser	Phe	Arg	Ile	Thr	Asn	Leu	Pro	Leu	Gln	Asp	625	630	635	640
Thr	Thr	Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Asn	Phe	Asn	Asp	Ile	645	650	655	
Ile	His	Ser	Ile	Ile	Asp	Met	Asp	Ala	Asp	Val	Met	Thr	Ile	Glu	Asn	660	665	670	
Ser	Arg	Ser	Ser	Glu	Lys	Leu	Leu	Ser	Val	Phe	Arg	Glu	Gly	Val	Lys	675	680	685	
Tyr	Gly	Ala	Gly	Ile	Gly	Pro	Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Arg	690	695	700	
Ile	Pro	Ser	Thr	Glu	Glu	Ile	Ala	Asp	Arg	Ile	Asn	Lys	Met	Leu	Ala	705	710	715	720
Val	Leu	Asp	Thr	Asn	Ile	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	725	730	735	
Thr	Arg	Lys	Tyr	Ala	Glu	Val	Lys	Pro	Ala	Leu	Glu	Asn	Met	Val	Ser	740	745	750	
Ala	Ala	Lys	Leu	Ile	Arg	Thr	Gln	Leu	Ala	Ser	Ala	Lys				755	760	765	

<210> 12

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 12

atccaacaat gtgagatgtc atgaattctg ac

32

<210> 13

<211> 32

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 13
 gtcagaattc atgacatctc acattggttg at 32

<210> 14
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
 ctcacggtcc gatgagaagc tcct 24

<210> 15
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 15
 gatcggtacc tcacttggag ctggcaagtt g 31

<210> 16
 <211> 1638
 <212> DNA
 <213> Zea mays

<400> 16
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 cgaaacccta gctcctctta cgccatggcc accgtgtcgc tcactccgca ggcggtcttc 120
 tccaccgagt ccggcggcgc cctggcctct gccaccatcc tccgcttccc gccaaacttc 180
 gtccgcctcc gcggcggcgg atgtcagcgc aattcctaac gctaagggtg cgcagccgtc 240
 cgccgtcgta ttggccgagc gtaacctgct cggctccgac gccagcctcg ccgtccacgc 300
 ggggggagagg ctgggaagaa ggatagccac ggatgctatc accacgccgg tagtgaacac 360
 gtccgcctac tgggtcaaca actcgcaaga gctaatacgc ttttaaggagg ggaggcatgc 420
 tagcttcgag tatgggaggt atgggaaccc gaccacggag gcattagaga agaagatgag 480
 cgcactggag aaagcagagt ccaccgtgtt tgtggcgtca gggatgtatg cagctgtggc 540
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 ctaagcactc taatcagttt gtattgacaa aatatgaggt gatggctgtc ttggatcttg 1500
 tcaagatctg tgacaatgat atgagctgat gactgcgaat aagttctctt ttgcttattt 1560

tatccgtcaa attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
 aaaaaaaaaa aactcgag 1638

<210> 17
 <211> 480
 <212> PRT
 <213> Zea mays

<400> 17
 Asn Ser Gly Ser Lys Pro Pro Arg Pro Asn Glu Arg Ser Val Pro Ser
 1 5 10 15
 Arg Ala Asp Ala Glu Thr Leu Ala Pro Leu Thr Pro Trp Pro Pro Cys
 20 25 30
 Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro Ala Ala Pro Trp
 35 40 45
 Pro Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser Ser Ala Ser Ala
 50 55 60
 Ala Ala Asp Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser
 65 70 75 80
 Ala Val Val Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu
 85 90 95
 Ala Val His Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala
 100 105 110
 Ile Thr Thr Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser
 115 120 125
 Gln Glu Leu Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr
 130 135 140
 Gly Arg Tyr Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser
 145 150 155 160
 Ala Leu Glu Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr
 165 170 175
 Ala Ala Val Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile
 180 185 190
 Val Thr Thr Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn
 195 200 205
 Glu Leu Pro Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp
 210 215 220
 Met Asp Ala Leu Gln Asn Ala Leu Asp Asn Asn Asn Val Ser Leu Phe
 225 230 235 240
 Phe Thr Glu Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu
 245 250 255
 His Val Ser Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp
 260 265 270

Ser	Thr	Phe	Ala	Ser	Pro	Ile	Asn	Gln	Lys	Ala	Leu	Thr	Leu	Gly	Ala	
		275					280					285				
Asp	Leu	Val	Ile	His	Ser	Ala	Thr	Lys	Tyr	Ile	Ala	Gly	His	Asn	Asp	
	290					295					300					
Val	Ile	Gly	Gly	Cys	Val	Ser	Gly	Arg	Asp	Glu	Leu	Val	Ser	Lys	Val	
305					310					315					320	
Arg	Ile	Tyr	His	His	Val	Val	Gly	Gly	Val	Leu	Asn	Pro	Asn	Ala	Ala	
				325					330					335		
Tyr	Leu	Ile	Leu	Arg	Gly	Met	Lys	Thr	Leu	His	Leu	Arg	Val	Gln	Cys	
			340					345					350			
Gln	Asn	Asp	Thr	Ala	Leu	Arg	Met	Ala	Gln	Phe	Leu	Glu	Glu	His	Pro	
		355					360					365				
Lys	Ile	Ala	Arg	Val	Tyr	Tyr	Pro	Gly	Leu	Pro	Ser	His	Pro	Glu	His	
	370					375					380					
His	Ile	Ala	Lys	Ser	Gln	Met	Thr	Gly	Phe	Gly	Gly	Val	Val	Ser	Phe	
385					390					395					400	
Glu	Val	Ala	Gly	Asp	Phe	Asp	Ala	Thr	Arg	Lys	Phe	Ile	Asp	Ser	Val	
				405					410					415		
Lys	Ile	Pro	Tyr	His	Ala	Pro	Ser	Phe	Gly	Gly	Cys	Glu	Ser	Ile	Ile	
			420					425					430			
Asp	Gln	Pro	Ala	Ile	Met	Ser	Tyr	Trp	Asp	Ser	Lys	Glu	Gln	Arg	Asp	
		435					440					445				
Ile	Tyr	Gly	Ile	Lys	Asp	Asn	Leu	Ile	Arg	Phe	Ser	Ile	Gly	Val	Glu	
	450					455					460					
Asp	Phe	Glu	Asp	Leu	Lys	Asn	Asp	Leu	Val	Gln	Ala	Leu	Glu	Lys	Ile	
465					470					475					480	

<210> 18
 <211> 3639
 <212> DNA
 <213> Zea mays

<400> 18																	
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caaacgacaa	atattcgaga	acgagatagt	ataatctata	ggataatcag	acatgtcctt		180										
agagggtgtt	tgtttagaat	tataatatgt	atagaatata	taatccaaca	aattttgaac		240										
taacaagt	aaaatttgat	agattatata	atctgggcac	attataatcc	ttaacaaaca		300										
ccatcttagt	aattttttat	ttagtgtctc	gtttggatgt	gaagaagatg	gagttgaata		360										
ccaaatcatg	tatgatactg	aaatgagatg	taattttaat	tctattgttt	ggatgtcgtt		420										
gaattggagt	ttgaagttat	gcggtctaat	tttacgcaat	accgagatga	gactttatac		480										
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gctccaaacg	aggtggagta	tttagaagta	gataagcgcc	tctgctgcac	gaagcgatga		660										
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gcaatatatt	gcagtactat	gccttattga	ttgggtatat	aaatgaattt	tagcacacag	3600
atagagcaga	agtaagacaa	attaacacaa	agttctaga			3639

<210> 19
 <211> 509
 <212> PRT
 <213> Zea mays

<400> 19
 Met Ala Thr Val Ser Leu Thr Pro Gln Ala Val Phe Ser Thr Glu Ser
 1 5 10 15
 Gly Gly Ala Leu Ala Ser Ala Thr Ile Leu Arg Phe Pro Pro Asn Phe
 20 25 30

His His Val Val Gly Gly Val Leu Asn Pro Asn Ala Ala Tyr Leu Ile
 355 360 365
 Leu Arg Gly Met Lys Thr Leu His Leu Arg Val Gln Cys Gln Asn Asp
 370 375 380
 Thr Ala Leu Arg Met Ala Gln Phe Leu Glu Glu His Pro Lys Ile Ala
 385 390 395 400
 Arg Val Tyr Tyr Pro Gly Leu Pro Ser His Pro Glu His His Ile Ala
 405 410 415
 Lys Ser Gln Met Thr Gly Phe Gly Gly Val Val Ser Phe Glu Val Ala
 420 425 430
 Gly Asp Phe Asp Ala Thr Arg Lys Phe Ile Asp Ser Val Lys Ile Pro
 435 440 445
 Tyr His Ala Pro Ser Phe Gly Gly Cys Glu Ser Ile Ile Asp Gln Pro
 450 455 460
 Ala Ile Met Ser Tyr Trp Asp Ser Lys Glu Gln Arg Asp Ile Tyr Gly
 465 470 475 480
 Ile Lys Asp Asn Leu Ile Arg Phe Ser Ile Gly Val Glu Asp Phe Glu
 485 490 495
 Asp Leu Lys Asn Asp Leu Val Gln Ala Leu Glu Lys Ile
 500 505

<210> 20

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 20

aattcatgag tgca

14

<210> 21

<211> 14

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 21

aatttgact catg

14

<210> 22

<211> 1350

<212> DNA

<213> Escherichia coli

<400> 22

atggctgaaa ttgttgtctc caaatttggc ggtaccagcg tagctgattt tgacgccatg 60
 aaccgcagcg ctgatattgt gctttctgat gccaacgtgc gtttagttgt cctctcggct 120

tctgctggta	tcactaatct	gctggctcgt	ttagctgaag	gactggaacc	tggcgagcga	180
ttcgaaaaac	tcgacgctat	ccgcaacatc	cagtttgcca	ttctggaacg	tctgcgttac	240
ccgaacgtta	tccgtgaaga	gattgaacgt	ctgctggaga	acattactgt	tctggcagaa	300
gcggcgggcg	tggcaacgtc	tccggcgctg	acagatgagc	tggtcagcca	cggcgagctg	360
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gatgtacgta	aagtgatgcg	taccaacgac	cgatttggtc	gtgcagagcc	agatatagcc	480
gcgctggcgg	aactggccgc	gctgcagctg	ctcccacgtc	tcaatgaagg	cttagtgatc	540
acccagggat	ttatcggtag	cgaaaataaa	ggtcgtacaa	cgacgcttgg	ccgtggaggc	600
agcgattata	cggcagcctt	gctggcgagg	gctttacacg	catctcgtgt	tgatatctgg	660
accgacgtcc	cgggcaccta	caccaccgat	ccacgcgtag	tttccgcagc	aaaacgcatt	720
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gaggtggaag	aaggtctggc	gctggctcgc	ttgattggca	atgacctgtc	aaaagcctgc	1200
gccgttggca	aagaggtatt	cggcgtactg	gaaccgttca	acattcgcat	gatttggttat	1260
ggcgcatcca	gccataacct	gtgcttctctg	gtgcccggcg	aagatgccga	gcaggtgggtg	1320
caaaaactgc	atagtaattt	gtttgagtaa				1350

<210> 23

<211> 449

<212> PRT

<213> Escherichia coli

<400> 23

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Val	Arg	Leu	Val	Val	Leu	Ser	Ala	Ser	Ala	Gly	Ile	Thr	Asn	Leu	Leu		35		40		45	
Val	Ala	Leu	Ala	Glu	Gly	Leu	Glu	Pro	Gly	Glu	Arg	Phe	Glu	Lys	Leu		50		55		60	
Asp	Ala	Ile	Arg	Asn	Ile	Gln	Phe	Ala	Ile	Leu	Glu	Arg	Leu	Arg	Tyr	65		70		75		80
Pro	Asn	Val	Ile	Arg	Glu	Glu	Ile	Glu	Arg	Leu	Leu	Glu	Asn	Ile	Thr		85		90		95	
Val	Leu	Ala	Glu	Ala	Ala	Ala	Leu	Ala	Thr	Ser	Pro	Ala	Leu	Thr	Asp		100		105		110	
Glu	Leu	Val	Ser	His	Gly	Glu	Leu	Met	Ser	Thr	Leu	Leu	Phe	Val	Glu		115		120		125	
Ile	Leu	Arg	Glu	Arg	Asp	Val	Gln	Ala	Gln	Trp	Phe	Asp	Val	Arg	Lys	130		135		140		
Val	Met	Arg	Thr	Asn	Asp	Arg	Phe	Gly	Arg	Ala	Glu	Pro	Asp	Ile	Ala	145		150		155		160
Ala	Leu	Ala	Glu	Leu	Ala	Ala	Leu	Gln	Leu	Leu	Pro	Arg	Leu	Asn	Glu		165		170		175	

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 24
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<210> 25
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 25
 gtaccgcaa atttggagac aacaatttca gccatg 36

<210> 26
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 26
 atggcagcca agatgcttgc attgttcgct 30

<210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
 gaatgcagca ccaacaaagg gttgctgtaa 30

<210> 28
 <211> 2123
 <212> DNA
 <213> Zea mays

<400> 28
 tctagagcct attaccatct ctactcacgg gtcgtagagg tggtagaggta ggctacagct 60
 ggtgacaatc ctactcaccc tttgtaatcc tctacggctc tacgcgtagt taattgggta 120
 gatgtcaacc ccctctctaa gtggcagtag tgggcttggt tatacctgct agtgccctggg 180
 gatgttctat ttttctagta gtgcttgatc aaacattgca tagtttgact tgggacaaac 240
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 aatcatttgt taaaaaagggt ttaattttgc tgctttcttt cgtaaatgtt gttttcacat 360
 tagattttct ttgtgttata tacactggat acatacaaat tcagttgcag tagtctctta 420
 atccacatca gctaggcata ctttagcaaa agcaaattac acaaactctag tgtgcctgtc 480
 gtcacattct caataaactc gtcattgttt actaaaagta ctttttcgaa gcatcatatt 540
 aatccgaaaa cagttaggga agtctccaaa tctgaccaa tgccaagtca tcgtccagct 600
 tatcagcatc caactttcag tttcgcattg gctagaaatt gtttttcac tacatggcca 660
 ttgttgactg catgcatcta taaataggac ctagacgac aatcgcaatc gcatatccac 720
 tattctctag gaagcaaggg aatcacatcg ccatggcagc caagatgttt gcattgtttg 780
 cgctcctagc tctttgtgca accgccacta gtgctacca tatcccaggg cacttgtcac 840
 cactactgat gccattggct accatgaacc catggatgca gtactgcatg aagcaacagg 900

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gggttgccaa cttgttagcg tggccgaccc tgatgctgca gcaactgttg gcctcaccgc 960
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ctagtatgat gccgccgatg atgatgccaa gcatgatttc accaatgacg atgccgagta 1140
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tgtatcttat attgttataa aaaatatctt ataatccatt tgtaatccta gtcatacata 1860
aattttgtta ttttaattta gttgtttcac tactacattg caaccattag tatcatgcag 1920
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cggtagaagt tctctcgtag attgtcagtc atcaggtagc caccaccata cacgcttgct 2040
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<210> 29
<211> 211
<212> PRT
<213> Zea mays

<400> 29

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Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
 1              5              10              15

Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
          20              25              30

Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
          35              40              45

Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
          50              55              60

Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
65              70              75              80

Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
          85              90              95

Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
          100              105              110

Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
          115              120              125

Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
          130              135              140

Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145              150              155              160

Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
          165              170              175

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Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
180 185 190

Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
195 200 205

Ala Ala Phe
210

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 30
atgaaccctt ggatgca 17

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 31
cccacagcaa tggcgat 17

<210> 32
<211> 639
<212> DNA
<213> Zea mays

<400> 32
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cttggatgca gtactgcatg aagcaacagg gggttgccaa cttgttagcg tggccgaccc 180
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 240
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 300
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa 360
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 420
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac 480
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 540
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atccccacca 600
tgttcttaca gcagcccttt gttggtgctg cattctaga 639

<210> 33
<211> 211
<212> PRT
<213> Zea mays

<400> 33
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1 5 10 15

Thr	Ala	Thr	Ser	Ala	Thr	His	Ile	Pro	Gly	His	Leu	Ser	Pro	Leu	Leu
			20					25					30		
Met	Pro	Leu	Ala	Thr	Met	Asn	Pro	Trp	Met	Gln	Tyr	Cys	Met	Lys	Gln
		35					40					45			
Gln	Gly	Val	Ala	Asn	Leu	Leu	Ala	Trp	Pro	Thr	Leu	Met	Leu	Gln	Gln
	50					55					60				
Leu	Leu	Ala	Ser	Pro	Leu	Gln	Gln	Cys	Gln	Met	Pro	Met	Met	Met	Pro
65					70					75					80
Gly	Met	Met	Pro	Pro	Met	Thr	Met	Met	Pro	Met	Pro	Ser	Met	Met	Pro
				85					90					95	
Ser	Met	Met	Val	Pro	Thr	Met	Met	Ser	Pro	Met	Thr	Met	Ala	Ser	Met
			100					105					110		
Met	Pro	Pro	Met	Met	Met	Pro	Ser	Met	Ile	Ser	Pro	Met	Thr	Met	Pro
		115					120					125			
Ser	Met	Met	Pro	Ser	Met	Ile	Met	Pro	Thr	Met	Met	Ser	Pro	Met	Ile
	130					135					140				
Met	Pro	Ser	Met	Met	Pro	Pro	Met	Met	Met	Pro	Ser	Met	Val	Ser	Pro
145					150					155					160
Met	Met	Met	Pro	Asn	Met	Met	Thr	Val	Pro	Gln	Cys	Tyr	Ser	Gly	Ser
				165					170					175	
Ile	Ser	His	Ile	Ile	Gln	Gln	Gln	Gln	Leu	Pro	Phe	Met	Phe	Ser	Pro
			180					185					190		
Thr	Ala	Met	Ala	Ile	Pro	Pro	Met	Phe	Leu	Gln	Gln	Pro	Phe	Val	Gly
		195					200					205			

Ala Ala Phe
210

<210> 34
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 34
ctagcccggg tac 13

<210> 35
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 35
ctaggtaccc ggg 13

<210> 36
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

 <400> 36
 ccacttcacg acccatatcc cagggcactt 30

 <210> 37
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

 <400> 37
 ttctatctag aatgcagcac caacaaaggg 30

 <210> 38
 <211> 579
 <212> DNA
 <213> Zea mays

 <400> 38
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 cttggatgca gtactgcatg aagcaacagg gggttgcca cttgttagcg tggccgaccc 120
 tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 180
 cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 240
 tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgcca 300
 gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 360
 tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atggtgtcac 420
 caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 480
 ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atcccaccca 540
 tgttcttaca gcagcccttt gttgggtgctg cattctaga 579

 <210> 39
 <211> 191
 <212> PRT
 <213> Zea mays

 <400> 39
 Met Thr His Ile Pro Gly His Leu Ser Pro Leu Leu Met Pro Leu Ala
 1 5 10 15
 Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln Gln Gly Val Ala
 20 25 30
 Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln Leu Leu Ala Ser
 35 40 45
 Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro Gly Met Met Pro
 50 55 60
 Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro Ser Met Met Val
 65 70 75 80

Pro	Thr	Met	Met	Ser	Pro	Met	Thr	Met	Ala	Ser	Met	Met	Pro	Pro	Met	
				85					90					95		
Met	Met	Pro	Ser	Met	Ile	Ser	Pro	Met	Thr	Met	Pro	Ser	Met	Met	Pro	
			100					105					110			
Ser	Met	Ile	Met	Pro	Thr	Met	Met	Ser	Pro	Met	Ile	Met	Pro	Ser	Met	
		115					120					125				
Met	Pro	Pro	Met	Met	Met	Pro	Ser	Met	Val	Ser	Pro	Met	Met	Met	Pro	
	130					135					140					
Asn	Met	Met	Thr	Val	Pro	Gln	Cys	Tyr	Ser	Gly	Ser	Ile	Ser	His	Ile	
145					150					155					160	
Ile	Gln	Gln	Gln	Gln	Leu	Pro	Phe	Met	Phe	Ser	Pro	Thr	Ala	Met	Ala	
				165					170					175		
Ile	Pro	Pro	Met	Phe	Leu	Gln	Gln	Pro	Phe	Val	Gly	Ala	Ala	Phe		
			180					185					190			

<210> 40

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 40

ctagaagcct cggcaacgtc agcaacggcg gaagaatccg gtg 43

<210> 41

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 41

catgcaccgg attcttccgc cgttgctgac gttgccgagg ctt 43

<210> 42

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 42

gatcccatgg cgccccttaa gtccaccgcc agcctccccg tcgcccgccg ctcct 55

<210> 43

<211> 55

<212> DNA

<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 43
 ctagaggagc ggcgggacgac ggggaggctg gcggtggact taaggggagc catgg 55

<210> 44
 <211> 59
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 44
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<210> 45
 <211> 59
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 45
 ttaagcccct ggaacggagc gacggcggtg gccgacgagg ccatcatcac ggtgggagc 59

<210> 46
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 46
 catggctggc ttccccacga ggaagaccaa caatgacatt acctccattg ctagcaacgg 60
 tggaagagta caatg 75

<210> 47
 <211> 75
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 47
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 cgtggggaag ccagc 75

<210> 48
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 48
 catggcttcc tcaatgatct cctccccagc tgttaccacc gtcaaccgtg ccggtgccgg 60
 catggttgct ccattcacgc gcctcaaaag 90

<210> 49
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 49
 catgcttttg aggccggtga atggagcaac catgccggca ccggcacggt tgacggtggt 60
 aacagctggg gaggagatca ttgaggaagc 90

<210> 50
 <211> 31
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 50
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<210> 51
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 51
 tactaaccat ggcttcctca 20

<210> 52
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 52
 ggccatggcc gc 12

<210> 53
 <211> 30
 <212> DNA
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<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 53
 gaaaccatgg ccagtgtgat tgcgcaggca 30

<210> 54
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 54
 gaaaggtacc ttacaacaac tgtgccagc 29

<210> 55
 <211> 1494
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (1461)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (1464)
 <223> n = A, C, G, or T

<220>
 <221> unsure
 <222> (1465)
 <223> n = A, C, G, or T

<400> 55
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 ggatgaggtt ttcttttctg ctaatgctgc tgccttggct tcaaggaagt cctccccaag 120
 ggtgataaat gaggctgtcc aaaaagccgc tgctgctctg aagggctctg atcatcggag 180
 ggccacaaat gttagtgccg gggtggatgc tcaacagaag aaattgaatc tttctgttct 240
 tccaacaact acaattggat ctttccctca aactgccgat cttagaagrg twcgycgtga 300
 attcaaggct aacaagatct ccgaggaaga gtatgthaag tcaattaagg aggaaattcg 360
 caaagttggt garcttcaag aagagcttga tattgatgtt cttgttcatg gagaaccaga 420
 gagaaatgat atggttgagt acttcgggtga rcaattgtca ggctttgcct tcacygttaa 480
 tgggtgggtg caatcctatg gttcccgttg ygtgaagcca ccratcatct atggtgatgt 540
 gagccgcca aagccaatga cygtcttctg gtcattctctg gctcagagct ttaccaagcg 600
 cccaatgaag ggaatgctta ccggtcctgt taccattctc aactggkcct ttgtwagaaa 660
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<210> 56
 <211> 753
 <212> PRT
 <213> Escherichia coli

<400> 56

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Arg	Glu	Leu	Lys	Lys	Ala	Gln	Glu	Ser	Tyr	Trp	Ala	Gly	Asn	Ser	Thr
			20					25					30		
Arg	Glu	Glu	Leu	Leu	Ala	Val	Gly	Arg	Glu	Leu	Arg	Ala	Arg	His	Trp
			35				40					45			
Asp	Gln	Gln	Lys	Gln	Ala	Gly	Ile	Asp	Leu	Leu	Pro	Val	Gly	Asp	Phe
	50					55					60				
Ala	Trp	Tyr	Asp	His	Val	Leu	Thr	Thr	Ser	Leu	Leu	Leu	Gly	Asn	Val
65					70					75					80
Pro	Ala	Arg	His	Gln	Asn	Lys	Asp	Gly	Ser	Val	Asp	Ile	Asp	Thr	Leu
				85					90					95	
Phe	Arg	Ile	Gly	Arg	Gly	Arg	Ala	Pro	Thr	Gly	Glu	Pro	Ala	Ala	Ala
			100					105					110		
Ala	Glu	Met	Thr	Lys	Trp	Phe	Asn	Thr	Asn	Tyr	His	Tyr	Met	Val	Pro
		115					120					125			
Glu	Phe	Val	Lys	Gly	Gln	Gln	Phe	Lys	Leu	Thr	Trp	Thr	Gln	Leu	Leu
	130					135					140				
Asp	Glu	Val	Asp	Glu	Ala	Leu	Ala	Leu	Gly	His	Lys	Val	Lys	Pro	Val
145					150					155					160
Leu	Leu	Gly	Pro	Val	Thr	Trp	Leu	Trp	Leu	Gly	Lys	Val	Lys	Gly	Glu
				165					170					175	
Gln	Phe	Asp	Arg	Leu	Ser	Leu	Leu	Asn	Asp	Ile	Leu	Pro	Val	Tyr	Gln
			180					185					190		
Gln	Val	Leu	Ala	Glu	Leu	Ala	Lys	Arg	Gly	Ile	Glu	Trp	Val	Gln	Ile
		195					200					205			
Asp	Glu	Pro	Ala	Leu	Val	Leu	Glu	Leu	Pro	Gln	Ala	Trp	Leu	Asp	Ala
	210					215					220				
Tyr	Lys	Pro	Ala	Tyr	Asp	Ala	Leu	Gln	Gly	Gln	Val	Lys	Leu	Leu	Leu
225					230					235					240
Thr	Thr	Tyr	Phe	Glu	Gly	Val	Thr	Pro	Asn	Leu	Asp	Thr	Ile	Thr	Ala
				245					250					255	
Leu	Pro	Val	Gln	Gly	Leu	His	Val	Asp	Leu	Val	His	Gly	Lys	Asp	Asp
			260					265					270		
Val	Ala	Glu	Leu	His	Lys	Arg	Leu	Pro	Ser	Asp	Trp	Leu	Leu	Ser	Ala
		275					280					285			

Gly 290	Leu	Ile	Asn	Gly	Arg	Asn 295	Val	Trp	Arg	Ala	Asp 300	Leu	Thr	Glu	Lys
Tyr 305	Ala	Gln	Ile	Lys	Asp 310	Ile	Val	Gly	Lys	Arg 315	Asp	Leu	Trp	Val	Ala 320
Ser	Ser	Cys	Ser	Leu 325	Leu	His	Ser	Pro	Ile 330	Asp	Leu	Ser	Val	Glu 335	Thr
Arg	Leu	Asp	Ala 340	Glu	Val	Lys	Ser	Trp 345	Phe	Ala	Phe	Ala	Leu 350	Gln	Lys
Cys	His	Glu 355	Leu	Ala	Leu	Leu	Arg 360	Asp	Ala	Leu	Asn 365	Ser	Gly	Asp	Thr
Ala 370	Ala	Leu	Ala	Glu	Trp	Ser 375	Ala	Pro	Ile	Gln	Ala 380	Arg	Arg	His	Ser
Thr 385	Arg	Val	His	Asn 390	Pro	Ala	Val	Glu	Lys	Arg 395	Leu	Ala	Ala	Ile	Thr 400
Ala	Gln	Asp	Ser	Gln 405	Arg	Ala	Asn	Val	Tyr 410	Glu	Val	Arg	Ala	Glu 415	Ala
Gln	Arg	Ala	Arg 420	Phe	Lys	Leu	Pro	Ala 425	Trp	Pro	Thr	Thr	Thr 430	Ile	Gly
Ser	Phe	Pro 435	Gln	Thr	Thr	Glu	Ile 440	Arg	Thr	Leu	Arg 445	Leu	Asp	Phe	Lys
Lys 450	Gly	Asn	Leu	Asp	Ala	Asn 455	Asn	Tyr	Arg	Thr	Gly 460	Ile	Ala	Glu	His
Ile 465	Lys	Gln	Ala	Ile	Val 470	Glu	Gln	Glu	Arg	Leu 475	Gly	Leu	Asp	Val	Leu 480
Val	His	Gly	Glu	Ala 485	Glu	Arg	Asn	Asp	Met 490	Val	Glu	Tyr	Phe	Gly 495	Glu
His	Leu	Asp	Gly 500	Phe	Val	Phe	Thr	Gln 505	Asn	Gly	Trp	Val	Gln 510	Ser	Tyr
Gly	Ser	Arg 515	Cys	Val	Lys	Pro	Pro 520	Ile	Val	Ile	Gly	Asp 525	Ile	Ser	Arg
Pro 530	Ala	Pro	Ile	Thr	Val	Glu 535	Trp	Ala	Lys	Tyr	Ala 540	Gln	Ser	Leu	Thr
Asp 545	Lys	Pro	Val	Lys	Gly 550	Met	Leu	Thr	Gly	Pro 555	Val	Thr	Ile	Leu	Cys 560
Trp	Ser	Phe	Pro	Arg 565	Glu	Asp	Val	Ser	Arg	Glu	Thr	Ile	Ala	Lys 575	Gln
Ile	Ala	Leu	Ala 580	Cys	Val	Met	Lys	Trp 585	Pro	Ile	Trp	Lys	Pro 590	Leu	Glu
Leu	Ala	Ser 595	Ser	Arg	Leu	Thr	Asn 600	Arg	Arg	Leu	Arg	Gln 605	Gly	Leu	Pro

Leu	Arg	Arg	Ser	Asp	Trp	Asp	Ala	Tyr	Leu	Gln	Trp	Gly	Val	Glu	Ala
610						615					620				
Phe	Arg	Ile	Asn	Ala	Ala	Val	Ala	Lys	Asp	Asp	Thr	Gln	Ile	His	Thr
625					630					635					640
His	Met	Cys	Tyr	Cys	Glu	Phe	Asn	Asp	Ile	Met	Asp	Ser	Ile	Ala	Ala
				645					650					655	
Leu	Asp	Arg	Asp	Val	Ile	Thr	Ile	Glu	Thr	Ser	Arg	Ser	Asp	Met	Glu
			660					665					670		
Leu	Leu	Glu	Ser	Phe	Glu	Glu	Phe	Asp	Tyr	Pro	Asn	Glu	Ile	Gly	Pro
		675					680					685			
Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Asn	Val	Pro	Ser	Val	Glu	Trp	Ile
	690					695					700				
Glu	Ala	Leu	Leu	Lys	Lys	Ala	Ala	Lys	Arg	Ile	Pro	Ala	Glu	Arg	Leu
705					710					715					720
Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	Thr	Arg	Gly	Trp	Pro	Glu	Thr
				725					730					735	
Arg	Ala	Ala	Leu	Ala	Asn	Met	Val	Gln	Ala	Ala	Gln	Asn	Leu	Arg	Arg
			740					745					750		

Gly

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Glu	Leu	Lys	Lys	Ala	Thr	Glu	Gly	Tyr	Trp	Asn	Gly	Lys	Ile	Thr	Val
			20					25					30		
Asp	Glu	Leu	Phe	Lys	Val	Gly	Lys	Asp	Leu	Arg	Thr	Gln	Asn	Trp	Lys
		35					40					45			
Leu	Gln	Lys	Glu	Ala	Gly	Val	Asp	Ile	Ile	Pro	Ser	Asn	Asp	Phe	Ser
	50					55					60				
Phe	Tyr	Asp	Gln	Val	Leu	Asp	Leu	Ser	Leu	Leu	Phe	Asn	Val	Ile	Pro
65					70					75					80
Asp	Arg	Tyr	Thr	Lys	Tyr	Asp	Leu	Ser	Pro	Ile	Asp	Thr	Leu	Phe	Ala
				85					90					95	
Met	Gly	Arg	Gly	Leu	Gln	Arg	Lys	Ala	Thr	Glu	Thr	Glu	Lys	Ala	Val
			100					105					110		
Asp	Val	Thr	Ala	Leu	Glu	Met	Val	Lys	Trp	Phe	Asp	Ser	Asn	Tyr	His
		115					120					125			

Tyr	Val	Arg	Pro	Thr	Phe	Ser	Lys	Thr	Thr	Gln	Phe	Lys	Leu	Asn	Gly
	130					135					140				
Gln	Lys	Pro	Val	Asp	Glu	Phe	Leu	Glu	Ala	Lys	Glu	Leu	Gly	Ile	His
145					150					155					160
Thr	Arg	Pro	Val	Leu	Leu	Gly	Pro	Val	Ser	Tyr	Leu	Phe	Leu	Gly	Lys
				165					170					175	
Ala	Asp	Lys	Asp	Ser	Leu	Asp	Leu	Glu	Pro	Leu	Ser	Leu	Leu	Glu	Gln
			180					185					190		
Leu	Leu	Pro	Leu	Tyr	Thr	Glu	Ile	Leu	Ser	Lys	Leu	Ala	Ser	Ala	Gly
		195					200					205			
Ala	Thr	Glu	Val	Gln	Ile	Asp	Glu	Pro	Val	Leu	Val	Leu	Asp	Leu	Pro
	210					215					220				
Ala	Asn	Ala	Gln	Ala	Ala	Ile	Lys	Lys	Ala	Tyr	Thr	Tyr	Phe	Gly	Glu
225					230					235					240
Gln	Ser	Asn	Leu	Pro	Lys	Ile	Thr	Leu	Ala	Thr	Tyr	Phe	Gly	Thr	Val
				245					250					255	
Val	Pro	Asn	Leu	Asp	Ala	Ile	Lys	Gly	Leu	Pro	Val	Ala	Ala	Leu	His
			260					265					270		
Val	Asp	Phe	Val	Arg	Ala	Pro	Glu	Gln	Phe	Asp	Glu	Val	Val	Ala	Ala
		275					280					285			
Ile	Gly	Asn	Lys	Gln	Thr	Leu	Ser	Val	Gly	Ile	Val	Asp	Gly	Arg	Asn
	290					295					300				
Ile	Trp	Lys	Asn	Asp	Phe	Lys	Lys	Ser	Ser	Ala	Ile	Val	Asn	Lys	Ala
305					310					315					320
Ile	Glu	Lys	Leu	Gly	Ala	Asp	Arg	Val	Val	Val	Ala	Thr	Ser	Ser	Ser
				325					330					335	
Leu	Leu	His	Thr	Pro	Val	Asp	Leu	Asn	Asn	Glu	Thr	Lys	Leu	Asp	Ala
			340					345					350		
Glu	Ile	Lys	Gly	Phe	Phe	Ser	Phe	Ala	Thr	Gln	Lys	Leu	Asp	Glu	Val
		355					360					365			
Val	Val	Ile	Thr	Lys	Asn	Val	Ser	Gly	Gln	Asp	Val	Ala	Ala	Ala	Leu
	370					375					380				
Glu	Ala	Asn	Ala	Lys	Ser	Val	Glu	Ser	Arg	Gly	Lys	Ser	Lys	Phe	Ile
385					390					395					400
His	Asp	Ala	Ala	Val	Lys	Arg	Arg	Val	Ala	Ser	Ile	Asp	Glu	Lys	Met
				405					410					415	
Ser	Thr	Arg	Ala	Ala	Pro	Phe	Glu	Gln	Arg	Leu	Pro	Glu	Gln	Gln	Lys
			420					425					430		
Val	Phe	Asn	Leu	Pro	Leu	Phe	Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro
		435					440					445			

Gln	Thr	Lys	Asp	Ile	Arg	Ile	Asn	Arg	Asn	Lys	Phe	Asn	Lys	Gly	Thr
450				455				460							
Ile	Ser	Ala	Glu	Glu	Tyr	Glu	Lys	Phe	Ile	Asn	Ser	Glu	Ile	Glu	Lys
465				470				475				480			
Val	Ile	Arg	Phe	Gln	Glu	Glu	Ile	Gly	Leu	Asp	Val	Leu	Val	His	Gly
				485				490				495			
Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	Phe	Gly	Glu	Gln	Ile	Asn
				500				505				510			
Gly	Tyr	Ala	Phe	Thr	Val	Asn	Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	Arg
				515				520				525			
Tyr	Val	Arg	Pro	Pro	Ile	Ile	Val	Gly	Asp	Leu	Ser	Arg	Pro	Lys	Ala
530				535				540							
Met	Ser	Val	Lys	Glu	Ser	Val	Tyr	Ala	Gln	Ser	Ile	Thr	Ser	Lys	Pro
545				550				555				560			
Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Ile	Thr	Cys	Leu	Arg	Trp	Ser	Phe
				565				570				575			
Pro	Arg	Asp	Asp	Val	Asp	Gln	Lys	Thr	Gln	Ala	Met	Gln	Leu	Ala	Leu
				580				585				590			
Ala	Leu	Arg	Asp	Glu	Val	Asn	Asp	Leu	Glu	Ala	Ala	Gly	Ile	Lys	Val
595				600				605							
Ile	Gln	Val	Asp	Glu	Pro	Ala	Leu	Arg	Glu	Gly	Leu	Pro	Leu	Arg	Glu
610				615				620							
Gly	Thr	Glu	Arg	Ser	Ala	Tyr	Tyr	Thr	Trp	Ala	Ala	Glu	Ala	Phe	Arg
625				630				635				640			
Val	Ala	Thr	Ser	Gly	Val	Ala	Asn	Lys	Thr	Gln	Ile	His	Ser	His	Phe
				645				650				655			
Cys	Tyr	Ser	Asp	Leu	Asp	Pro	Asn	His	Ile	Lys	Ala	Leu	Asp	Ala	Asp
660				665				670							
Val	Val	Ser	Ile	Glu	Phe	Ser	Lys	Lys	Asp	Asp	Ala	Asn	Tyr	Ile	Ala
675				680				685							
Glu	Phe	Lys	Asn	Tyr	Pro	Asn	His	Ile	Gly	Leu	Gly	Leu	Phe	Asp	Ile
690				695				700							
His	Ser	Pro	Arg	Ile	Pro	Ser	Lys	Asp	Glu	Phe	Ile	Ala	Lys	Ile	Ser
705				710				715				720			
Thr	Ile	Leu	Lys	Ser	Tyr	Pro	Ala	Glu	Lys	Phe	Trp	Val	Asn	Pro	Asp
				725				730				735			
Cys	Gly	Leu	Lys	Thr	Arg	Gly	Trp	Glu	Glu	Thr	Arg	Leu	Ser	Leu	Thr
740				745				750							
His	Met	Val	Glu	Ala	Ala	Lys	Tyr	Phe	Arg	Glu	Gln	Tyr	Lys	Asn	
755				760				765							

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 Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Gly Lys Ser Ser Ala Glu
 20 25 30
 Asp Leu Lys Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
 35 40 45
 Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Xaa Asn Thr Phe Ser Tyr
 50 55 60

Tyr	Asp	Gln	Val	Leu	Asp	Thr	Thr	Ala	Met	Leu	Gly	Ala	Val	Pro	Ala	65	70	75	80
Arg	Tyr	Asn	Trp	Ala	Gly	Gly	Glu	Ile	Ala	Phe	Asp	Thr	Tyr	Phe	Ser	85	90	95	
Met	Ala	Arg	Gly	Asn	Xaa	Ser	Val	Pro	Ala	Met	Glu	Met	Thr	Lys	Trp	100	105	110	
Xaa	Asp	Thr	Asn	Tyr	His	Phe	Ile	Val	Pro	Glu	Leu	Gly	Pro	Asp	Val	115	120	125	
Asn	Phe	Ser	Tyr	Ala	Ser	His	Lys	Ala	Val	Asp	Glu	Tyr	Lys	Glu	Ala	130	135	140	
Lys	Gly	Leu	Gly	Val	Asp	Thr	Val	Pro	Val	Leu	Ile	Gly	Pro	Val	Ser	145	150	155	160
Tyr	Leu	Leu	Leu	Ser	Lys	Pro	Ala	Lys	Gly	Val	Glu	Lys	Ser	Phe	Pro	165	170	175	
Leu	Leu	Ser	Leu	Leu	Asp	Lys	Val	Leu	Pro	Ile	Tyr	Lys	Glu	Val	Ile	180	185	190	
Ala	Glu	Leu	Lys	Ala	Ala	Gly	Ala	Ser	Trp	Ile	Gln	Phe	Asp	Glu	Pro	195	200	205	
Thr	Leu	Val	Leu	Asp	Leu	Gln	Ala	His	Gln	Leu	Glu	Ala	Phe	Thr	Lys	210	215	220	
Ala	Tyr	Ala	Glu	Leu	Glu	Ser	Ser	Leu	Ser	Gly	Leu	Asn	Val	Leu	Thr	225	230	235	240
Glu	Thr	Tyr	Phe	Ala	Asp	Val	Pro	Ala	Glu	Ala	Phe	Lys	Thr	Leu	Thr	245	250	255	
Ala	Leu	Lys	Gly	Val	Thr	Ala	Phe	Gly	Phe	Asp	Leu	Val	Arg	Gly	Ala	260	265	270	
Gln	Thr	Leu	Asp	Leu	Ile	Lys	Gly	Gly	Phe	Pro	Ser	Gly	Lys	Tyr	Leu	275	280	285	
Phe	Ala	Gly	Val	Val	Asp	Gly	Arg	Asn	Ile	Trp	Ala	Asn	Asp	Leu	Ala	290	295	300	
Ala	Ser	Leu	Asn	Leu	Leu	Gln	Ser	Leu	Glu	Gly	Ile	Val	Gly	Lys	Asp	305	310	315	320
Lys	Leu	Val	Val	Ser	Thr	Ser	Cys	Ser	Leu	Leu	His	Thr	Ala	Val	Asp	325	330	335	
Leu	Val	Asn	Glu	Thr	Lys	Leu	Asp	Asp	Glu	Ile	Lys	Ser	Trp	Leu	Ala	340	345	350	
Phe	Ala	Ala	Gln	Lys	Val	Val	Glu	Val	Asn	Ala	Leu	Ala	Lys	Ala	Leu	355	360	365	
Ala	Xaa	His	Lys	Asp	Glu	Ala	Phe	Phe	Ser	Ala	Asn	Ala	Thr	Ala	Gln	370	375	380	

Ala	Ser	Arg	Lys	Ser	Ser	Pro	Arg	Val	Thr	Asn	Glu	Ala	Val	Gln	Lys	385	390	395	400
Ala	Ala	Ala	Ala	Leu	Lys	Gly	Ser	Asp	His	Arg	Arg	Ala	Thr	Asn	Val	405	410	415	
Ser	Ser	Arg	Leu	Asp	Ala	Gln	Gln	Lys	Lys	Leu	Asn	Leu	Pro	Val	Leu	420	425	430	
Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Val	Glu	Leu	Arg	Arg	435	440	445	
Val	Arg	Arg	Glu	Tyr	Lys	Ala	Lys	Lys	Ile	Ser	Glu	Glu	Glu	Tyr	Val	450	455	460	
Lys	Ala	Ile	Lys	Ala	Glu	Ile	Lys	Lys	Val	Val	Asp	Leu	Gln	Glu	Glu	465	470	475	480
Leu	Asp	Ile	Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	485	490	495	
Val	Glu	Tyr	Phe	Gly	Glu	Gln	Leu	Ser	Gly	Phe	Ala	Phe	Thr	Ala	Asn	500	505	510	
Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Lys	Pro	Pro	Ile	Ile	515	520	525	
Tyr	Gly	Asp	Val	Ser	Arg	Pro	Asn	Pro	Met	Thr	Val	Phe	Trp	Ser	Lys	530	535	540	
Thr	Ala	Gln	Ser	Met	Thr	Lys	Arg	Pro	Met	Lys	Gly	Met	Leu	Thr	Gly	545	550	555	560
Pro	Val	Thr	Ile	Leu	Asn	Trp	Ser	Phe	Val	Arg	Asn	Asp	Gln	Pro	Arg	565	570	575	
Xaa	Glu	Thr	Cys	Tyr	Gln	Ile	Ala	Xaa	Xaa	Ile	Lys	Asp	Glu	Val	Glu	580	585	590	
Asp	Leu	Glu	Lys	Ala	Xaa	Ile	Thr	Val	Ile	Gln	Ile	Asp	Glu	Ala	Ala	595	600	605	
Leu	Arg	Glu	Gly	Leu	Pro	Leu	Arg	Lys	Ala	Glu	His	Ala	Phe	Tyr	Leu	610	615	620	
Asn	Trp	Ala	Val	His	Ser	Phe	Arg	Ile	Thr	Asn	Val	Gly	Ile	Gln	Asp	625	630	635	640
Thr	Thr	Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Asn	Phe	Asn	Asp	Ile	645	650	655	
Ile	His	Ser	Ile	Ile	Asp	Met	Asp	Ala	Asp	Val	Ile	Thr	Ile	Glu	Asn	660	665	670	
Ser	Arg	Ser	Asp	Glu	Lys	Leu	Leu	Ser	Val	Phe	Arg	Glu	Gly	Val	Lys	675	680	685	
Tyr	Gly	Ala	Gly	Ile	Gly	Pro	Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Arg	690	695	700	

Ile	Pro	Ser	Thr	Glu	Glu	Ile	Ala	Asp	Arg	Val	Asn	Lys	Met	Leu	Ala
705					710					715					720
Val	Leu	Asp	Thr	Asn	Ile	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys
				725					730					735	
Thr	Arg	Lys	Tyr	Ala	Glu	Val	Lys	Pro	Ala	Leu	Glu	Asn	Met	Val	Ser
			740					745					750		
Ala	Ala	Lys	Ala	Ile	Arg	Thr	Gln	Leu	Ala	Ser	Ser	Lys			
		755					760					765			

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 <213> Zea mays

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 Xaa Val Arg Ile Gln Glu Glu Leu Asp Ile Asp Val Val Val His Gly
 20 25 30
 Glu Pro Glu Arg Xaa Asp Xaa Xaa Xaa Tyr Phe Gly Glu Xaa Leu Ser
 35 40 45
 Ala Phe Ala Ser Thr Ala Thr Gly Trp Xaa Xaa Ser Tyr Gly Ser Arg
 50 55 60

<210> 60
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 Ser Gly Gln Lys Asp Glu Val Phe Phe Ser Ala Asn Ala Ala Ala Leu
 20 25 30
 Ala Ser Arg Lys Ser Ser Pro Arg Val Ile Asn Glu Ala Val Gln Lys
 35 40 45
 Ala Ala Ala Ala Leu Lys Gly Ser Asp His Arg Arg Ala Thr Asn Val
 50 55 60

Ser	Ala	Arg	Leu	Asp	Ala	Gln	Gln	Lys	Lys	Leu	Asn	Leu	Ser	Val	Leu	65	70	75	80
Pro	Thr	Thr	Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Ala	Asp	Leu	Arg	Arg	85	90	95	
Val	Arg	Arg	Glu	Phe	Lys	Ala	Asn	Lys	Ile	Ser	Glu	Glu	Glu	Tyr	Val	100	105	110	
Lys	Ser	Ile	Lys	Glu	Glu	Ile	Arg	Lys	Val	Val	Glu	Leu	Gln	Glu	Glu	115	120	125	
Leu	Asp	Ile	Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	130	135	140	
Val	Glu	Tyr	Phe	Gly	Glu	Gln	Leu	Ser	Gly	Phe	Ala	Phe	Thr	Val	Asn	145	150	155	160
Gly	Trp	Val	Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Lys	Pro	Pro	Ile	Ile	165	170	175	
Tyr	Gly	Asp	Val	Ser	Arg	Pro	Lys	Pro	Met	Thr	Val	Phe	Trp	Ser	Ser	180	185	190	
Leu	Ala	Gln	Ser	Phe	Thr	Lys	Arg	Pro	Met	Lys	Gly	Met	Leu	Thr	Gly	195	200	205	
Pro	Val	Thr	Ile	Leu	Asn	Trp	Xaa	Phe	Val	Arg	Asn	Asp	Gln	Pro	Arg	210	215	220	
Ser	Glu	Thr	Thr	Tyr	Gln	Ile	Ala	Leu	Ala	Ile	Lys	Asp	Glu	Val	Glu	225	230	235	240
Asp	Leu	Glu	Lys	Ala	Gly	Ile	Thr	Val	Ile	Gln	Ile	Asp	Glu	Ala	Ala	245	250	255	
Leu	Arg	Glu	Gly	Leu	Pro	Leu	Xaa	Lys	Ser	Glu	Gln	Ala	His	Tyr	Leu	260	265	270	
Asp	Trp	Ala	Val	His	Ala	Phe	Arg	Ile	Thr	Asn	Val	Gly	Val	Gln	Asp	275	280	285	
Thr	Thr	Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Asn	Phe	Asn	Asp	Ile	290	295	300	
Ile	His	Ser	Ile	Ile	Asp	Met	Asp	Ala	Asp	Val	Ile	Thr	Ile	Glu	Asn	305	310	315	320
Ser	Arg	Ser	Asp	Glu	Lys	Leu	Leu	Ser	Val	Phe	Arg	Glu	Gly	Val	Lys	325	330	335	
Tyr	Gly	Ala	Gly	Ile	Xaa	Pro	Gly	Val	Tyr	Asp	Ile	His	Ser	Pro	Arg	340	345	350	
Ile	Pro	Pro	Thr	Glu	Glu	Ile	Ala	Asp	Arg	Ile	Asn	Lys	Met	Leu	Ala	355	360	365	
Val	Leu	Glu	Lys	Asn	Ile	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	370	375	380	

Thr	Arg	Lys	Tyr	Thr	Glu	Val	Lys	Pro	Ala	Leu	Thr	Asn	Met	Val	Ala
385					390					395					400
Ala	Ala	Lys	Leu	Ile	Arg	Asn	Glu	Leu	Ala	Lys					
				405						410					